

Figure 1:
HBM haplotype indicated with crosshatch

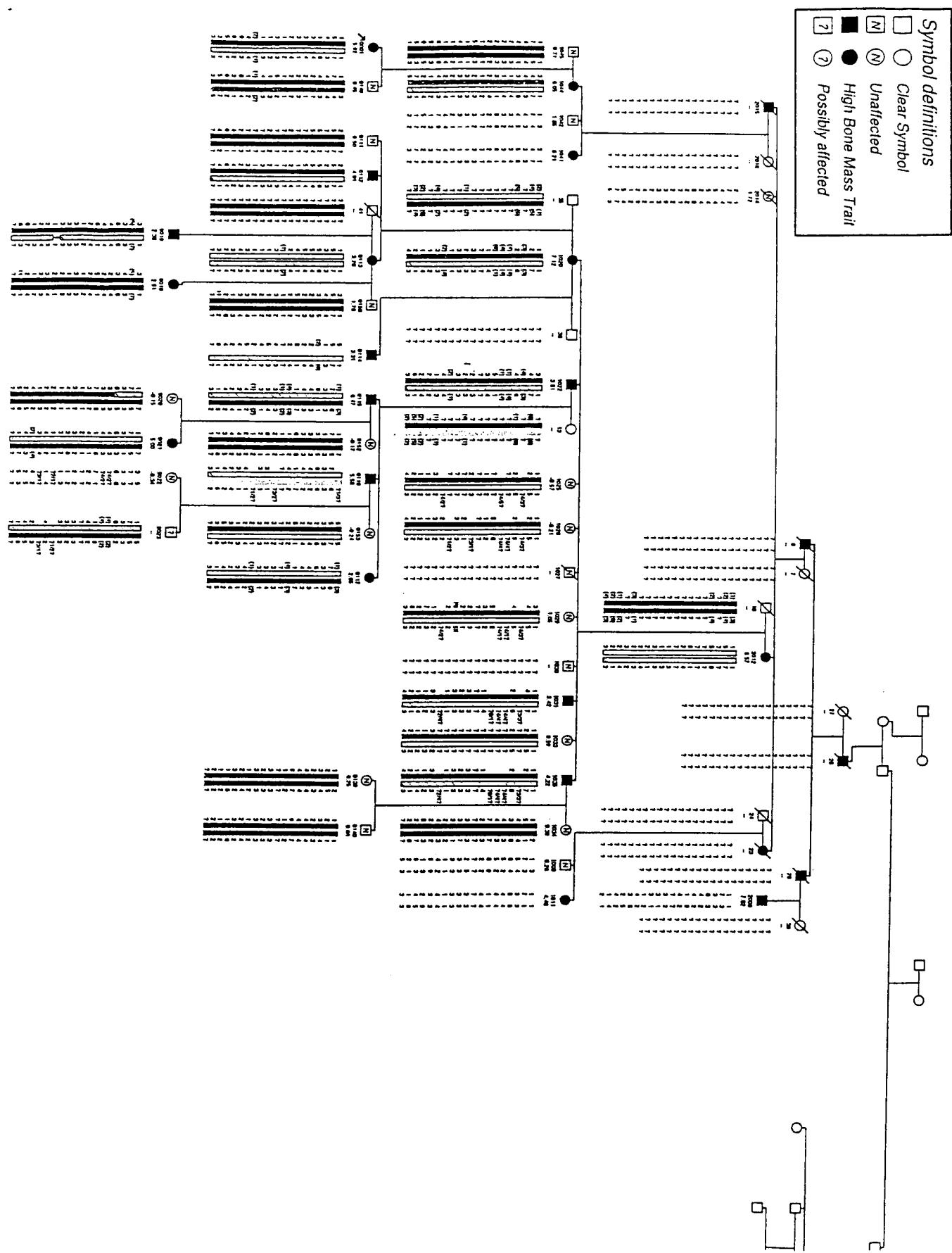
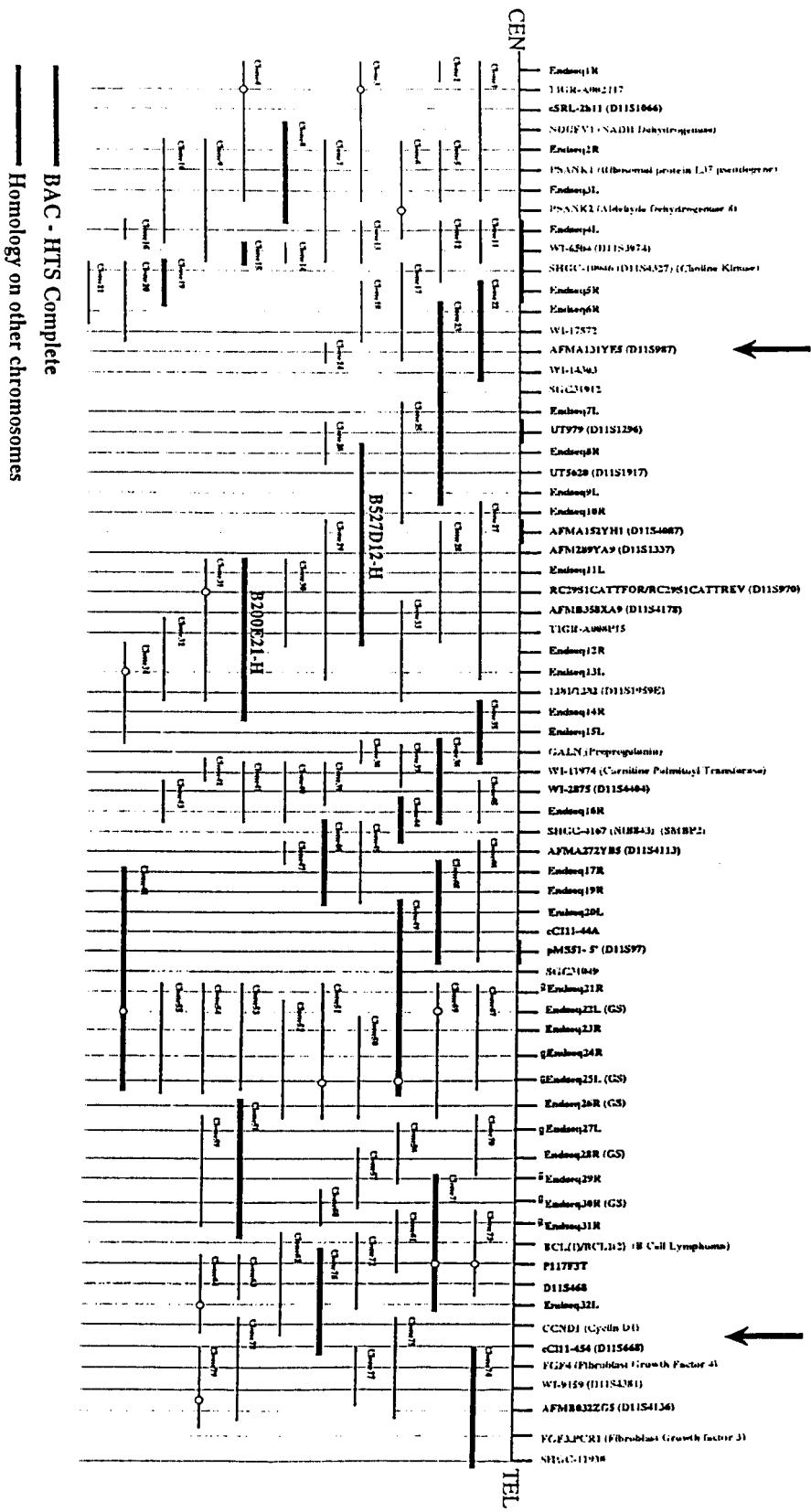


Figure 2

EST/C_{cute}
Anonymous STS
STSs From BAC Ends

Genetic Marker

BAC/STS Map of the HBM Region



Exon 1

ACTAAAGGCCGCCGCCGCCATGGAGCCCGAGTGAGCGCGCGCG
GCCCGTCCGCCGCCGACAACATGGAGGCAGCGCCGCCGGCGC
GTGGCCGCTGCTGCTGCTGCTGCTGGCGCTGTGCGCTGC
CCGGCCCCGCCGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549

gccccacagCCTCGCCGCTCCTGCTATTGCCAACCGCCGGACGTACGGCTG
GTGGACGCCGGCGGAGTCAGACTGGAGTCCACCATCGTGGTCAGCGGCC
TGGAGGATGCGGCCGCACTGGACTTCCAGTTCCAAGGGAGCCGTGTA
CTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAG
ACGGGGGCCGCGTGCAGAACGTGGTCATCTCCGGCTGGTCTCTCCCG
ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTC
AGAGACCAACCGCATCGAGGTGGCAACCTCAATGGCACATCCCAGGAAG
GTGCTCTTCTGGCAGGACCTTGACCAGCCAGGGCATCGCCTGGACC
CCGCTCACGGtaaacccctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945

ccccgtcacagGTACATGTACTGGACAGACTGGGGTGAGACGCCCGGATTGA
GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGAC
ATTTACTGGCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCT
ACTGGGCTGACGCCAAGCTCAGCTTCAATCCACCGTGCCAACCTGGACGG
CTCGTTCCGgttaggtaccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850

tccctgactgcagGCAGAAGGTGGAGGGCAGCCTGACGCACCCCTCGCCC
TGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTC
CATCCATGCCTGCAACAAGCGCACTGGGGGAAGAGGAAGGAGATCCTG
AGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGC
AGCCTTCTgtgagtgccgg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088

tttctcagTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGT
GCCTGCTGTCCCCAAGCGAGCCTTCTACACATGCGCCTGCCACGGG
TGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggtggacg

FIGURE 3A

... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100

ctccacagGAGCCGAGGAGGTGCTGCTGGCTGCCCGGCGGACGGACCTACGG
AGGATCTCGCTGGACACGCCGGACTCACCGACATCGTGCAGGTGG
ACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTA
TGTCTACTGGACAGATGACGAGGTGCGGCCATCGCAGGGCGTACCTG
GACGGGTCTGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCG
ATGGCATCGCGGTGACTGGGTGGCCCACCGCTACTGGACCGACAC
GGGCACGGACCGCATCGAGGTGACGCCTCAACGGCACCTCCGCAAG
ATCCTGGTGTGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACC
CCGTGATGGGtaagacggc

..... 3211 nt

Exon 7 Coordinates: 527d12_Contig309G 11311-11482

ttcttcctccagCCTCATGTACTGGACAGACTGGGGAGAGAACCCCTAAAATCGAGT
GTGCCAACTGGATGGCAGGAGCGGGCTGTGCTGGTCAATGCCCTCC
CGGGTGGCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTAC
TGGGGAGACGCCAAGACAGACAAGATCGAGtgaggctctgtgg

..... 13445 nt

Exon 8 Coordinates: 527d12_Contig309G 24927-25143

ccgtcctgcagGTGATCAATGTTGATGGGACGAAGAGGGCGGACCCCTCCTGGAG
GACAAGCTCCCGCACATTTCGGGTTCACGCTGCTGGGGACTTCATCTA
CTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAG
GCCAGCCGGGACGTCATCATTGACCAGCTGCCGACCTGATGGGCTCA
AAGCTGTGAATGTGGCCAAGGTCGTCGgtgagtccgggggtc

....2826 nt

Exon 9 Coordinates: 527d12_Contig309G 27969-28256

gttcgcttcagGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGAGCCACC
TGTGCTTCTTCACACCCCCACGCAACCCGGTGTGGCTGCCCATCGGCCT
GGAGCTGCTGAGTGACATGAAGACCTGCATCGCCTGAGGCCTTCTG
GTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATA
ACAACGACGTGGCCATCCCGCTCACGGCGTCAAGGAGGCCTCAGCCCT
GGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTAGCCTGA
AGtagcgtggc

.....3102.....

FIGURE 3B

Exon 10 Coordinates: 527d12_Contig309G 31358-31582

cctgctgccagACCATCAGCCGCCTTCATGAACGGGAGCTCGGTGGAGCAC
GTGGTGGAGTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA
TGGGCAAGAACCTCTACTGGGCCACACTGGGACCAACAGAATCGAAGT
GGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTG
GACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGtaagtgttgccctgtc

.....1297 nt.....

Exon 11 Coordinates: 527d12_Contig309G 32879-33064

gtgcctccagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGGATCGTG
CGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGG
GCCGGGCCAACGACCTCACCATGACTACGCTGACCAGCGCCTCTACTG
GACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGgtgagggcc
ggcct

.....2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454

gtgtcatgcagGTCAGGAGCGGGTCGTATTGCCGACGATCTCCGCACCCGT
TCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTG
CACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGAAACCGCACCCCTCA
TCCAGGGCCACCTGGACTTCGTATGGACATCCTGGTGTCCACTCCTCC
CGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGC
AGCTGTGCCTGCCATCCCCGGGCCACCGCTGCGGCTGCGCCTCACCA
CTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCGtaagtgcctcatgtt

.....2006 nt.....

Exon 13 Coordinates: 527d12_Contig309G 37460-37659

gcctcctctaCGCCCACCACTTCTGCTGTTAGCCAGAAATCTGCCATCAGT
CGGATGATCCCGGACGACCAGCACAGCCGGATCTCATCCTGCCCTGC
ATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTT
CATCTACTGGGTGGATGGCGCCAGAACATCAAGCGAGCCAAGGACGAC
GGGACCCAGgcaggtgcctgtgg

.....6965 nt.....

FIGURE 3C

Exon 14 Coordinates: 527d12_Contig309G 44624-44832

ctttgttacagCCCTTGTGACCTCTTGAGCCAAGGCCAAACCCAGACA
GGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTG
GACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAA
GCCATGGGGTGGTGCCTGCGTGGGACCGCGACAAGCCCAGGGCCATC
GTCGTCAACCGCGAGCGAGGgtaggaggccaac

.....1404 nt.....

Exon 15 Coordinates: 527d12_Contig309G 46236-46427

ccaccctcccgagGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGA
TCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGT CCTCTTCACAC
CGGCCTCATCCGCCCTGTGGCCCTGGTGGACAACACACTGGGCAAG
CTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGT
CAGgtacgcggccgg

.....686 nt.....

Exon 16 Coordinates: 527d12_Contig309G 47113-47322

ggctgttcgagGGGCCAACCGCTGACCTGGAGGACGCCAACATCGTGCAGC
CTCTGGGCCTGACCATCCTGGCAAGCATCTACTGGATCGACCGCCA
GCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGACAAGCGGACT
CGCATCCAGGGCCGTGTCGCCACCTCACTGGCATCCATGCAGTGGAGG
AAGTCAGCCTGGAGGGAGTTCTgtacgtggggc

.....3884 nt.....

Exon 17 Coordinates: 527d12_Contig309G 51206-51331

ttgtcttgagCAGCCCACCATGTGCCGTGACAATGGTGGCTGCTCCCACAT
CTGTATTGCCAACGGGTGATGGGACACCACGGTGCTCATGCCAGTCCAC
CTCGTGCCTGCAGAACCTGCTGACCTGTGGAGgtaggtgtgacctagggtgc

....3905 nt.....

Exon 18 Coordinates: 527d12_Contig309G 55236-55472

gttctctgtccctccccagAGCCGCCACCTGCTCCCCGGACCAGTTGCATGTGC
CACAGGGGAGATCGACTGTATCCCCGGGCCTGGCGCTGTGACGGCTTT
CCCGAGTGCATGACCAAGAGCGACGAGGAGGGCTGCCCGTGTGCTCCG
CCGCCAGTTCCCTGCGCGCGGGGTCAAGTGTGTGGACCTGCGCCTGCG
CTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGT
GACGgtgaggccctcc

.....3052 nt.....

FIGURE 3D

Exon 19 Coordinates: 527d12_Contig309G 58524-58634

tctccttcgcagCCATCTGCCTGCCAACCAACCAGTTCCGGTGTGCGAGCGGCCAGTG
TGTCTCATCAAACAGCAGTGCAGTCCTCCCCGACTGTATCGACGGCT
CCGACGAGCTCATGTGTGgtgagccagtt

.....1448 nt.....

Exon 20 Coordinates: 527d12_Contig309G 60082-60319

gtttgtctctggcagAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCCACAGC
AGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTTCGTATGGG
TGGTGTCTATTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCCGGGG
GCCAACGGGCCCTTCCCACGAGTATGTCAGCGGGACCCGCACGTGC
CCCTCAATTCAATAGCCCCGGCGGTTCCCAGCATGGCCCCTCACAGgtta
aggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552

cttccctcccgAGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGA
TGGGGGGCCGGGGCGGGGTGCCCTCTACGACCGGAACCACGTACAG
GGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCC
Ggtgagggcggg

.....6513 nt.....

Exon 22 Coordinates: 527d12_Contig309G 68065-68162

ttggctctccctcagATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG
TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACC
GTACAGgttaggacatcccctcag

.....2273 nt.....

FIGURE 3E

Exon 23 Coordinates: 527d12_Contig309G 70435-70901

tcaaacattccggccactgcgagaccgtacagGCCCTACATCATTGGAGGAATGGCGCCCC
GACGACGCCCTGCAGCACCGACGTGTGACAGCGACTACAGCGCCAGC
CGCTGGAAGGCCAGCAAGTACTACCTGGATTGAACACTCGGACTCAGACC
CCTATCCACCCCCACCCACGCCACAGCCAGTACCTGTCGGCGGAGGA
CAGCTGCCGCCCTGCCGCCACCGAGAGGGAGCTACTTCCATCTCTTC
CCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGCCA
CTCTGGCTTCTCTGTGCCCTGTAAATAGTTAAATATGAACAAAGAAAAAA
ATATATTATGATTAAAAATAAATATAATTGGGATTTAAAAACATGAGA
AATGTGAACTGTGATGGGGTGGGCAGGGCTGGAGAACTTGTACAGTGGAG
AAATATTATAAACTTAATTGTAAAACA

FIGURE 3F

Figure 4

Model for a LDL Receptor-Related protein, Zmax1

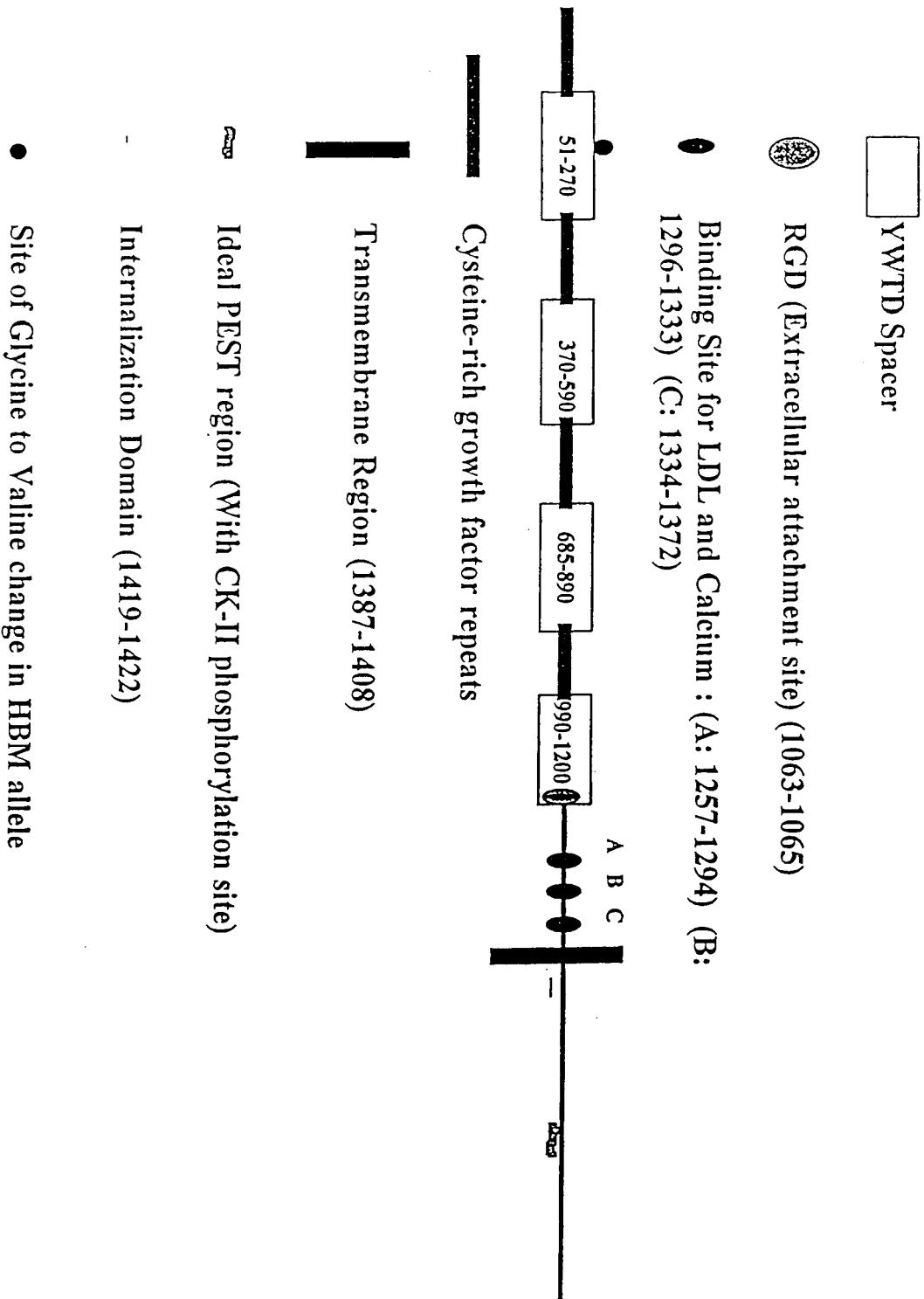
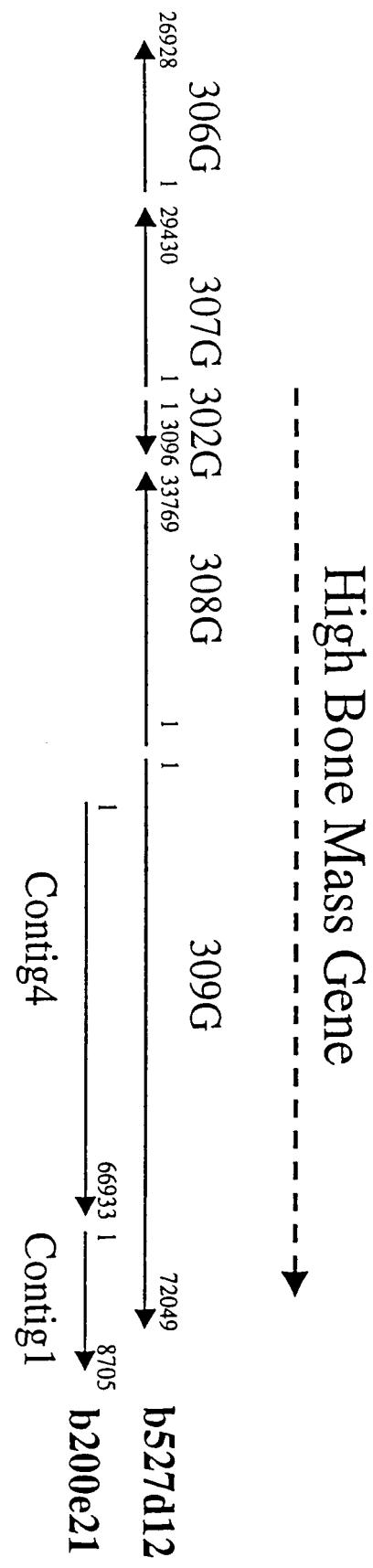


Figure 5



1	ACTAAAGCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGCGCGGGCCCCGTCCGGCC	60
61	GCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCTGCCGCTGCTGCTGCTGCT	120
1	M E A A P P G P P W P L L L L L L	17
121	GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCGCCGCGGCCCTGCCGCTCCTGCTATT	180
18	L L L A L C G C P A P A A A S P L L L F	37
181	TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGAGTCAGCTGGAGTCCACCAT	240
38	A N R R D V R L V D A G G V K L E S T I	57
241	CGTGGTCAGCGGCCTGGAGGGATGCGGCCGCGAGTGGACTTCCAGTTCCAAGGGAGCCGT	300
58	V V S G L E D A A A V D F Q F S K G A V	77
301	GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGC	360
78	Y W T D V S E E A I K Q T Y L N Q T G A	97
361	CGCCGTGCAGAACGTGGTCATCTCCGGCTGGTCTCTCCGACGGCCTGCCCTGCGACTG	420
98	A V Q N V V I S G L V S P D G L A C D W	117
421	GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCAACCT	480
118	V G K K L Y W T D S E T N R I E V A N L	137
481	CAATGGCACATCCCGGAAGGTGCTCTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC	540
138	N G T S R K V L F W Q D L D Q P R A I A	157
541	CTTGGACCCCGCTCACGGTACATGTACTGGACAGACTGGGGTGAGACGCCCGGATTGA	600
158	L D P A H G Y M Y W T D W G E T P R I E	177
601	GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGGACTCGGACATTACTGGCC	660
178	R A G M D G S T R K I I V D S D I Y W P	197
661	CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGCTGACGCCAAGCTCAG	720
198	N G L T I D L E E Q K L Y W A D A K L S	217
721	CTTCATCCACCGTGCCAACCTGGACGGCTCGTCCGGCAGAAGGTGGAGGGCAGCCT	780
218	F I H R A N L D G S F R Q K V V E G S L	237
781	GACGCACCCCTCGCCCTGACGCTCTCGGGGACACTCTGTACTGGACAGACTGGCAGAC	840
238	T H P F A L T L S G D T L Y W T D W Q T	257
841	CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGAAGAGGAAGGAGATCCTGAGTGC	900
258	R S I H A C N K R T G G K R K E I L S A	277
901	CCTCTACTCACCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTCTTCCACAC	960
278	L Y S P M D I Q V L S Q E R Q P F F H T	297
961	TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCCTGCTGCCCCAACGCGAGCC	1020
298	R C E E D N G G C S H L C L L S P S E P	317
1021	TTTCTACACATGCCTGCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTA	1080
318	F Y T C A C P T G V Q L Q D N G R T C K	337
1081	GGCAGGAGCCGAGGAGGTGCTGCTGGCCCGCGGACGGACCTACGGAGGATCTCGCT	1140
338	A G A E E V L L L A R R T D L R R I S L	357

Figure 6A

1141	GGACACGCCGGACTTCACCGACATCGTGCAGGTGGACGACATCCGGCACGCCATTGC	1200
358	D T P D F T D I V L Q V D D I R H A I A	377
1201	CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCAT	1260
378	I D Y D P L E G Y V Y W T D D E V R A I	397
1261	CCGCAGGGCGTACCTGGACGGGTCTGGGCGCAGACGCTGGTCAACACCGAGATCAACGA	1320
398	R R A Y L D G S G A Q T L V N T E I N D	417
1321	CCCCGATGGCATCGCGGTCGACTGGGTGGCCCAAACCTCTACTGGACCGACACGGCAC	1380
418	P D G I A V D W V A R N L Y W T D T G T	437
1381	GGACCGCATCGAGGTGACGCCCTAACGGCACCTCCCGCAAGATCCTGGTGTGGAGGA	1440
438	D R I E V T R L N G T S R K I L V S E D	457
1441	CCTGGACGAGCCCCGAGCCATCGCACTGCACCCGTGATGGGCCTCATGTACTGGACAGA	1500
458	L D E P R A I A L H P V M G L M Y W T D	477
1501	CTGGGGAGAGAACCCCTAAAATCGAGTGTGCCAACTGGATGGCAGGAGCGGGGTGTGCT	1560
478	W G E N P K I E C A N L D G Q E R R V L	497
1561	GGTCAATGCCTCCCTGGGTGGCCAACGGCCTGGCCCTGGACCTGCAGGAGGGAAAGCT	1620
498	V N A S L G W P N G L A L D L Q E G K L	517
1621	CTACTGGGGAGACCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG	1680
518	Y W G D A K T D K I E V I N V D G T K R	537
1681	GC GGACCCCTCCTGGAGGACAAGCTCCGCACATTTCGGGTTCACGCTGCTGGGGACTT	1740
538	R T L L E D K L P H I F G F T L L G D F	557
1741	CATCTACTGGACTGACTGGCAGCGCCGAGCATCGAGCGGTGCACAAGGTCAAGGCCAG	1800
558	I Y W T D W Q R R S I E R V H K V K A S	577
1801	CCGGGACGTTCATTGACCAGCTGCCGACCTGATGGGCTCAAAGCTGTGAATGTGGC	1860
578	R D V I I D Q L P D L M G L K A V N V A	597
1861	CAAGGTCGTCGGAACCAACCGTGTGGACAGGAACGGGGGTGCAGCCACCTGTGCTT	1920
598	K V V G T N P C A D R N G G C S H L C F	617
1921	CTTCACACCCACGCAACCGGTGTGGCTGCCCATGGCCTGGAGCTGCTGAGTGACAT	1980
618	F T P H A T R C G C P I G L E L L S D M	637
1981	GAAGACCTGCATCGTGCCTGAGGCCTTCTGGCTTCACCAAGCAGAGCCGCCATCCACAG	2040
638	K T C I V P E A F L V F T S R A A I H R	657
2041	GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCCTCACGGCGTCAAGGAGGC	2100
658	I S L E T N N N D V A I P L T G V K E A	677
2101	CTCAGCCCTGGACTTGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA	2160
678	S A L D F D V S N N H I Y W T D V S L K	697
2161	GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGAGTTGGCCT	2220
698	T I S R A F M N G S S V E H V V E F G L	717

Figure 6B

2221	TGACTACCCCGAGGCATGGCGTTGACTGGATGGCAAGAACCTCTACTGGGCCACAC	2280
718	D Y P E G M A V D W M G K N L Y W A D T	737
2281	TGGGACCAACAGAACATCGAAGTGGCGCGCTGGACGGCAGTTCCGGCAAGTCCTCGTGTG	2340
738	G T N R I E V A R L D G Q F R Q V L V W	757
2341	GAGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG	2400
758	R D L D N P R S L A L D P T K G Y I Y W	777
2401	GACCGAGTGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT	2460
778	T E W G G K P R I V R A F M D G T N C M	797
2461	GACGCTGGTGGACAAGGTGGCCGGCCAACGACCTCACCATTGACTACGCTGACCAGCG	2520
798	T L V D K V G R A N D L T I D Y A D Q R	817
2521	CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAAGGA	2580
818	L Y W T D L D T N M I E S S S N M L G Q E	837
2581	GC GGCGTGTGATTGCCGACGATCTCCCGCACCCGTTGGTCTGACGCAGTACAGCGATTA	2640
838	R V V I A D D L P H P F G L T Q Y S D Y	857
2641	TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG	2700
858	I Y W T D W N L H S I E R A D K T S G R	877
2701	GAACCGCACCCCATCCAGGGCACCTGGACTCGTGTGATGGACATCCTGGTGTCCACTC	2760
878	N R T L I Q G H L D F V M D I L V F H S	897
2761	CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGCAGCTGTG	2820
898	S R Q D G L N D C M H N N G Q C G Q L C	917
2821	CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCCTGGACCCAG	2880
918	L A I P G G H R C G C A S H Y T L D P S	937
2881	CAGCCGCAACTGCAGCCGCCACCCACCTTCTGCTGTTAGCCAGAAATCTGCCATCAG	2940
938	S R N C S P P T T F L L F S Q K S A I S	957
2941	TCGGATGATCCCGGACGACCAGCACAGCCGGATCTCATCCTGCCCTGCATGGACTGAG	3000
958	R M I P D D Q H S P D L I L P L H G L R	977
3001	GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGCG	3060
978	N V K A I D Y D P L D K F I Y W V D G R	997
3061	CCAGAACATCAAGCGAGCCAAGGACGACGGACCCAGCCCTTGACCTCTCTGAG	3120
998	Q N I K R A K D D G T Q P F V L T S L S	1017
3121	CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC	3180
1018	Q G Q N P D R Q P H D L S I D I Y S R T	1037
3181	ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCACAGGCTGAGCGGGGAAGC	3240
1038	L F W T C E A T N T I N V H R L S G E A	1057
3241	CATGGGGGTGGTGTGCGTGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA	3300
1058	M G V V L R G D R D K P R A I V V N A E	1077

Figure 6C

3301	GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACCGCGCAGC	3360
1078	R G Y L Y F T N M Q D R A A K I E R A A	1097
3361	CCTGGACGGCACCGAGCGCGAGGTCTCTTCACCACCGGCCATCCGCCCTGTGGCCCT	3420
1098	L D G T E R E V L F T T G L I R P V A L	1117
3421	GGTGGTGGACAACACACACTGGCAAGCTGTTGGTGGACGCGGACTGAAAGCGCATTGA	3480
1118	V V D N T L G K L F W V D A D L K R I E	1137
3481	GAGCTGTGACCTGTCAGGGGCCAACCGCTGACCCCTGGAGGACGCCAACATCGTCAGCC	3540
1138	S C D L S G A N R L T L E D A N I V Q P	1157
3541	TCTGGCCTGACCATCCTGGCAAGCATCTACTGGATCGACCGCCAGCAGCAGATGAT	3600
1158	L G L T I L G K H L Y W I D R Q Q Q M I	1177
3601	CGAGCGTGTGGAGAAGACCACCGGGACAAGCGGACTCGCATCCAGGGCGTGTGCCA	3660
1178	E R V E K T T G D K R T R I Q G R V A H	1197
3661	CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTCTCAGCCCACCCATG	3720
1198	L T G I H A V E E V S L E E F S A H P C	1217
3721	TGCCCGTGACAATGGTGGCTGCTCCACATCTGTATTGCCAAGGGTATGGACACCAAG	3780
1218	A R D N G G C S H I C I A K G D G T P R	1237
3781	GTGCTCATGCCAGTCCACCTCGTGCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC	3840
1238	C S C P V H L V L L Q N L L T C G E P P	1257
3841	CACCTGCTCCCCGGACCAGTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGC	3900
1258	T C S P D Q F A C A T G E I D C I P G A	1277
3901	CTGGCGCTGTGACGGCTTCCCGAGTGCATGCCAGAGCGACGAGGAGGGCTGCCGT	3960
1278	W R C D G F P E C D D Q S D E E G C P V	1297
3961	GTGCTCCGCCGCCAGTTCCCTGCGCGGGGTCACTGTGTGGACCTGCCCTGCCGT	4020
1298	C S A A Q F P C A R G Q C V D L R L R C	1317
4021	CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATG	4080
1318	D G E A D C Q D R S D E V D C D A I C L	1337
4081	GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGCCTCATCAAACAGCAGTGC	4140
1338	P N Q F R C A S G Q C V L I K Q Q C D S	1357
4141	CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATACCAAGCCGCC	4200
1358	F P D C I D G S D E L M C E I T K P P S	1377
4201	AGACGACAGCCGGCCACAGCAGTGCATCGGGCCCGTCAATTGGCATCATCCTCTCT	4260
1378	D D S P A H S S A I G P V I G I I L S L	1397
4261	CTTCGTATGGGTGTCTATTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCCGG	4320
1398	F V M G G V Y F V C Q R V V C Q R Y A G	1417
4321	GGCCAACGGGCCCTCCCGCACGAGTATGTCAGCGGGACCCGCACGTGCCCTCAATT	4380
1418	A N G P F P H E Y V S G T P H V P L N F	1437

Figure 6D

4381	CATAGCCCCGGCGGTTCCAGCATGGCCCCTCACAGGCATCGCATGCGAAAGTCCAT	4440
1438	I A P G G S Q H G P F T G I A C G K S M	1457
4441	GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGTGCCTCTACGACCGGAACCA	4500
1458	M S S V S L M G G R G G V P L Y D R N H	1477
4501	CGTCACAGGGGCCCTCGTCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCAT	4560
1478	V T G A S S S S S S T K A T L Y P P I	1497
4561	CCTGAACCCGCCCGCCCTCCCCGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA	4620
1498	L N P P P S P A T D P S L Y N M D M F Y	1517
4621	CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTGAGGAATGGC	4680
1518	S S N I P A T A R P Y R P Y I I R G M A	1537
4681	GCCCCCGACGACGCCCTGCAGCACCGACGTGTGACAGCGACTACAGGCCAGCCGCTG	4740
1538	P P T T P C S T D V C D S D Y S A S R W	1557
4741	GAAGGCCAGCAAGTACTACCTGGATTGAACTCGGACTCAGACCCCTATCCACCCCCCACC	4800
1558	K A S K Y Y L D L N S D S D P Y P P P P	1577
4801	CACGCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCGCCCTGCCGCCACCGA	4860
1578	T P H S Q Y L S A E D S C P P S P A T E	1597
4861	GAGGAGCTACTTCCATCTTCCGCCCTCCGTCCCCCTGCACGGACTCATCCTGACC	4920
1598	R S Y F H L F P P P S P C T D S S	1615
4921	TCGGCCGGCCACTCTGGCTTCTGTGCCCTGTAAATAGTTTAAATATGAACAAAGA	4980
4981	AAAAAAATATATTATGATTAAAAATAATATAATTGGGATTTAAAAACATGAGAAA	5040
5041	TGTGAACGTGATGGGTGGCAGGGCTGGGAGAACTTGTACAGTGGAGAAATATTAT	5100
5101	AAACTTAATTTGTAAAACA 5120	

Figure 6E

Northern Blot Analysis - Zmax 1

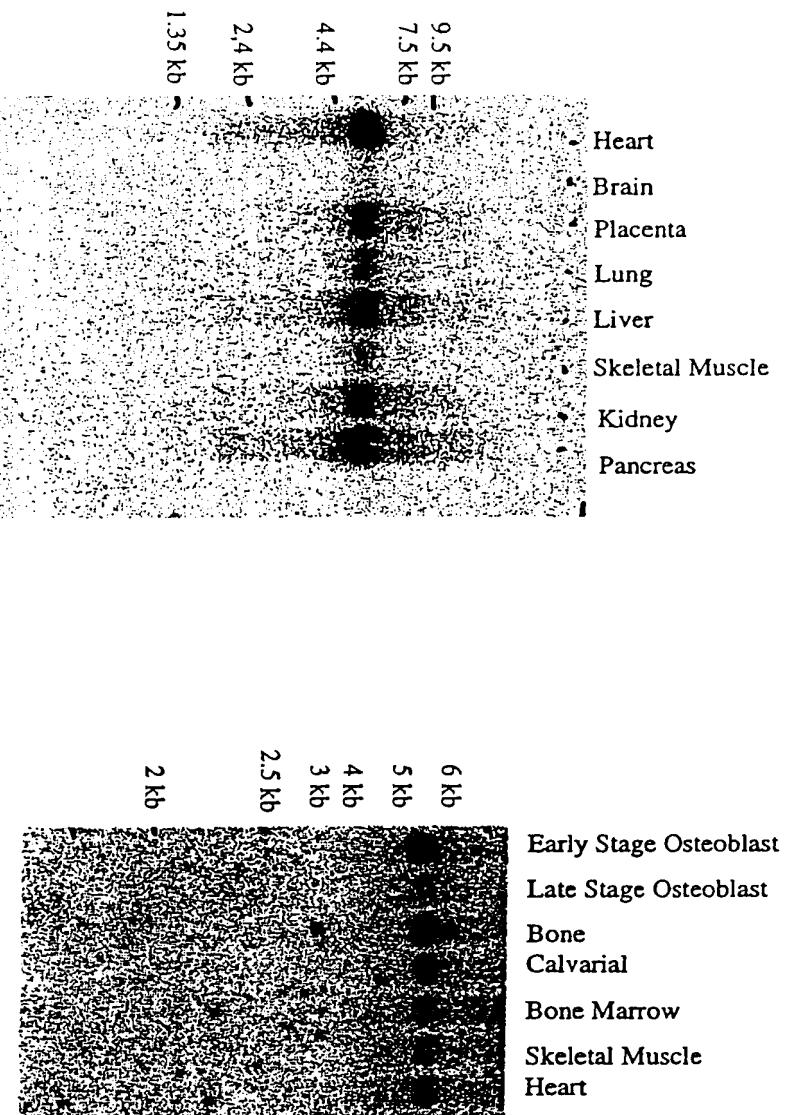
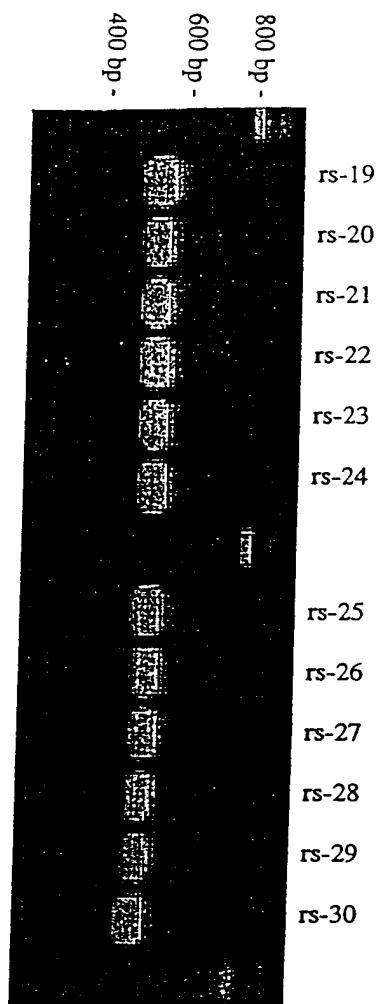


Figure 8

Zmax 1 random samples

b527d12-h_Contig087C_1.nt



ASO Detection of the Zmax1 Exon 3 Mutation

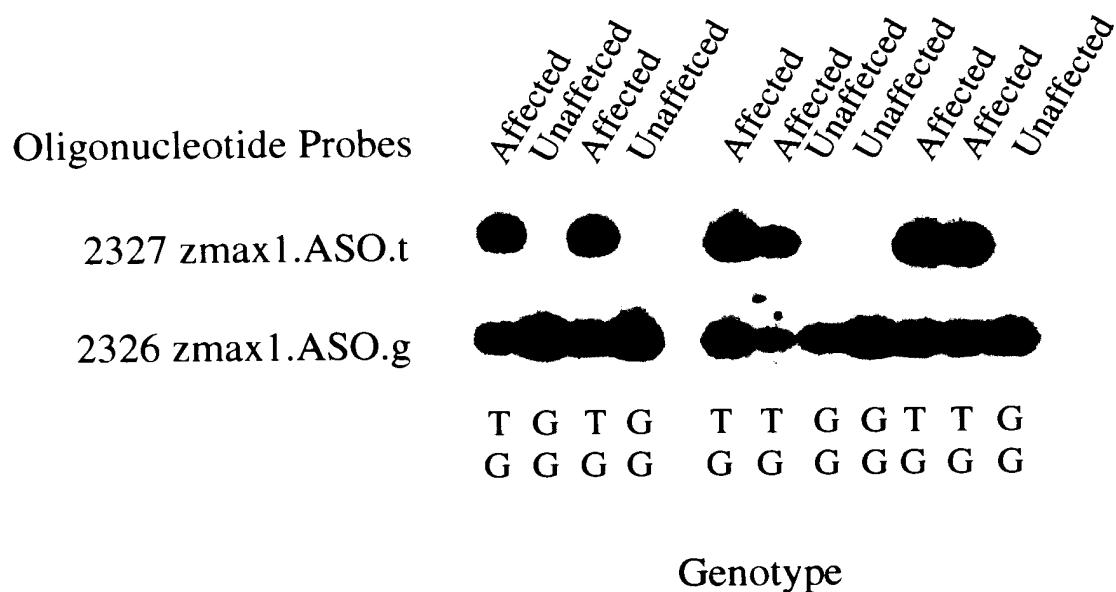


FIG. 9

Mouse Zmax1 In situ hybridization
100X Magnification

Antisense probe

Proliferating
chondrocytes

Osteoblasts
and osteoclasts

Growth
Plate

Proximal
aspect

Metaphysis

Sense probe

FIG. 10

Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts
and osteoclasts

Trabecular
bone

Proximal
Metaphysis



Sense probe



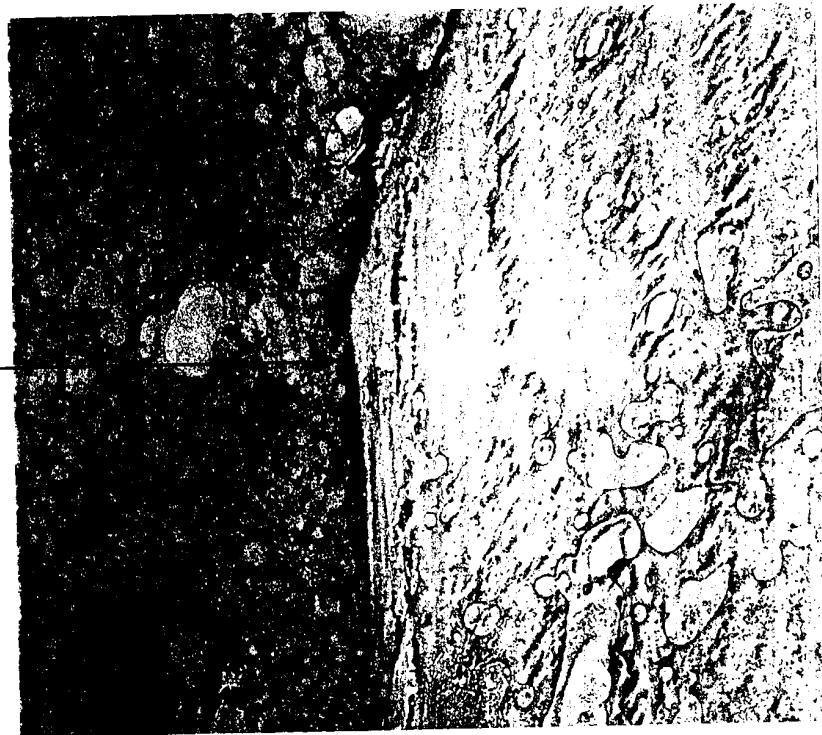
FIG. 11

Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts

Endosteum



Sense probe



FIG. 12

Antisense Inhibition of Zmax1 Expression

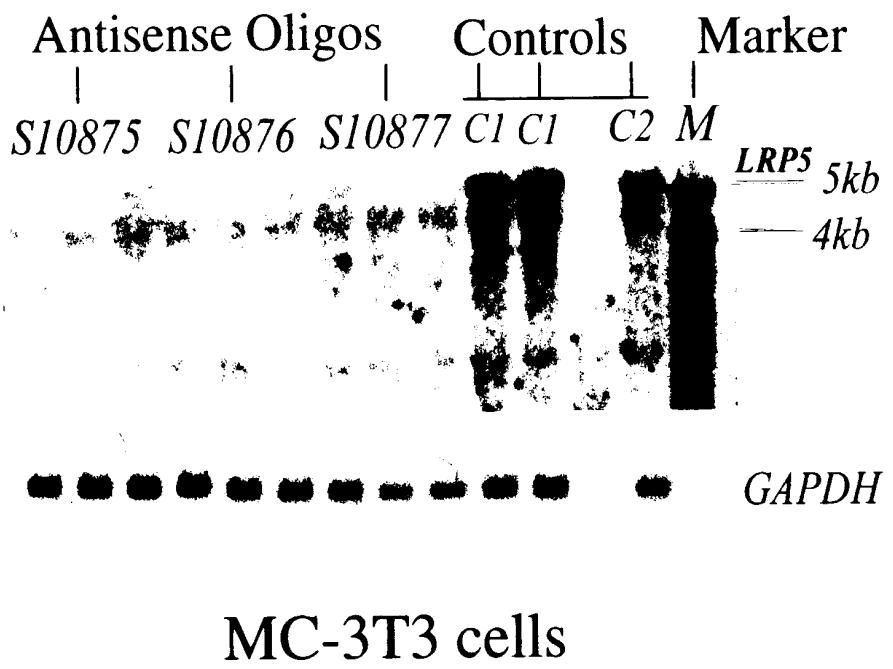


FIG. 13